SEQUENCE LISTING

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     Nilsson, Magnus
     Morisson, Veronique

<120> Cysteine Protease Inhibitors

<130> 1718-0195P

<150> US 60/252,840
<151> 2000-11-17

<150> PCT/GB00/01894
<151> 2000-05-18

<150> GB9911417.5
<151> 1999-05-18

<160> 4

<170> PatentIn version 3.0

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<223> Primer for cDNA of cysteinyl proteinase (Falcipain 2)

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<223> PCR product from amplification using primers for the cDNA sequenc
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aac aaa tat ctt agt tta aga tct tca aaa cca tta aag aat tct aaa   95
Asn Lys Tyr Leu Ser Leu Arg Ser Ser Lys Pro Leu Lys Asn Ser Lys
                20   25   30

tat tta tta gat caa atg aat tat gaa gaa gtt ata aaa aaa tat aga   143
Tyr Leu Leu Asp Gln Met Asn Tyr Glu Glu Val Ile Lys Lys Tyr Arg
            35   40   45

gga gaa gaa aat ttc gat cat gca gct tac gac tgg aga tta cac agt   191
Gly Glu Glu Asn Phe Asp His Ala Ala Tyr Asp Trp Arg Leu His Ser

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              50                   55                   60
ggt gta aca cct gta aag gat caa aaa aat tgt gga tct tgc tgg gcc      239
Gly Val Thr Pro Val Lys Asp Gln Lys Asn Cys Gly Ser Cys Trp Ala
        65                   70                   75

ttt agt agt ata ggt tcc gta gaa tca caa tat gct atc aga aaa aat      287
Phe Ser Ser Ile Gly Ser Val Glu Ser Gln Tyr Ala Ile Arg Lys Asn
80                   85                   90                   95

aaa tta ata acc tta agt gaa caa gaa tta gta gat tgt tca ttt aaa      335
Lys Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys Ser Phe Lys
                    100                  105                  110

aat tat ggt tgt aat gga ggt ctc att aat aat gcc ttt gag gat atg      383
Asn Tyr Gly Cys Asn Gly Gly Leu Ile Asn Asn Ala Phe Glu Asp Met
                115                  120                  125

att gaa ctt gga ggt ata tgt cca gat ggt gat tat cca tat gtg agt      431
Ile Glu Leu Gly Gly Ile Cys Pro Asp Gly Asp Tyr Pro Tyr Val Ser
            130                  135                  140

gat gct cca aat tta tgt aac ata gat aga tgt act gaa aaa tat gga      479
Asp Ala Pro Asn Leu Cys Asn Ile Asp Arg Cys Thr Glu Lys Tyr Gly
        145                  150                  155

atc aaa aat tat tta tcc gta cca gat aat aaa tta aaa gaa gca ctt      527
Ile Lys Asn Tyr Leu Ser Val Pro Asp Asn Lys Leu Lys Glu Ala Leu
160                  165                  170                  175

aga ttc ttg gga cct att agt att agt gta gcc gta tca gat gat ttt      575
Arg Phe Leu Gly Pro Ile Ser Ile Ser Val Ala Val Ser Asp Asp Phe
                180                  185                  190

gct ttt tac aaa gaa ggt att ttc gat gga gaa tgt ggt gat gaa tta      623
Ala Phe Tyr Lys Glu Gly Ile Phe Asp Gly Glu Cys Gly Asp Glu Leu
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aat cat gcc gtt atg ctt gta ggt ttt ggt atg aaa gaa att gtt aat      671
Asn His Ala Val Met Leu Val Gly Phe Gly Met Lys Glu Ile Val Asn
            210                  215                  220

cca tta acc aag aaa gga gaa aaa cat tat tat tat ata att aag aac      719
Pro Leu Thr Lys Lys Gly Glu Lys His Tyr Tyr Tyr Ile Ile Lys Asn
        225                  230                  235

tca tgg gga caa caa tgg gga gaa aga ggt ttc ata aat att gaa aca .    767
Ser Trp Gly Gln Gln Trp Gly Glu Arg Gly Phe Ile Asn Ile Glu Thr
240                  245                  250                  255

gat gaa tca gga tta atg aga aaa tgt gga tta ggt act gat gca ttc      815
Asp Glu Ser Gly Leu Met Arg Lys Cys Gly Leu Gly Thr Asp Ala Phe
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Val Thr Pro Val Lys Asp Gln Lys Asn Cys Gly Ser Cys Trp Ala Phe
65              70              75              80

Ser Ser Ile Gly Ser Val Glu Ser Gln Tyr Ala Ile Arg Lys Asn Lys
            85              90              95

Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys Ser Phe Lys Asn
        100             105             110

Tyr Gly Cys Asn Gly Gly Leu Ile Asn Asn Ala Phe Glu Asp Met Ile
        115             120             125

Glu Leu Gly Gly Ile Cys Pro Asp Gly Asp Tyr Pro,Tyr Val Ser Asp
    130             135             140

Ala Pro Asn Leu Cys Asn Ile Asp Arg Cys Thr Glu Lys Tyr Gly Ile
145             150             155             160

Lys Asn Tyr Leu Ser Val Pro Asp Asn Lys Leu Lys Glu Ala Leu Arg
            165             170             175

Phe Leu Gly Pro Ile Ser Ile Ser Val Ala Val Ser Asp Asp Phe Ala
        180             185             190

Phe Tyr Lys Glu Gly Ile Phe Asp Gly Glu Cys Gly Asp Glu Leu Asn
        195             200             205

His Ala Val Met Leu Val Gly Phe Gly Met Lys Glu Ile Val Asn Pro
    210             215             220

Leu Thr Lys Lys Gly Glu Lys His Tyr Tyr Tyr Ile Ile Lys Asn Ser
225             230             235             240

Trp Gly Gln Gln Trp Gly Glu Arg Gly Phe Ile Asn Ile Glu Thr Asp
            245             250             255

Glu Ser Gly Leu Met Arg Lys Cys Gly Leu Gly Thr Asp Ala Phe Ile
        260             265             270

Pro Leu Ile Glu His His His His His His
    275             280
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